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 RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/757,982

DATE: 07/30/2001  
 TIME: 12:32:42

Input Set : N:\Crf3\RULE60\09757982.txt  
 Output Set: N:\CRF3\07302001\I757982.raw

3 <110> APPLICANT: Acton, Susan  
 5 <120> TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
 7 <130> FILE REFERENCE: MNI-050  
 9 <140> CURRENT APPLICATION NUMBER: 09/757,982  
 10 <141> CURRENT FILING DATE: 2001-01-10  
 12 <150> PRIOR APPLICATION NUMBER: 09/163,115  
 13 <151> PRIOR FILING DATE: 1998-09-29  
 16 <160> NUMBER OF SEQ ID NOS: 15  
 18 <170> SOFTWARE: PatentIn Ver. 2.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 4137  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: 'n' at positions 2872, 3597 and 3682 may be any nucleic acid  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (297)..(1202)  
 32 <400> SEQUENCE: 1  
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 35 actccggacg cgcctcgca gtcgcagggt gggtgccccg cgccctgcagc gtccggccgg 120  
 37 gcggcgccgc gggaggtggc cgacaggctc cgggcctcgc agcctcagcc cccggcccag 180  
 39 cgcgcttcc gacggcgccg ccgcgccgag ccacccgccc gcccaaggtc tctcgccggc 240  
 41 gggagaacgg aaaactccca acttcctgag ttctaaagtt cctgttgctt cagaca atg 299  
 42 Met  
 43 1  
 45 gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347  
 46 Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln  
 47 5 10 15  
 49 cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395  
 50 Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn  
 51 20 25 30  
 53 ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443  
 54 Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr  
 55 35 40 45  
 57 aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa gtg 491  
 58 Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val  
 59 50 55 60 65  
 61 cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539  
 62 Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile Lys  
 63 70 75 80  
 65 gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa tat 587  
 66 Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys Tyr  
 67 85 90 95  
 69 tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa cta 635  
 70 Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu  
 71 100 105 110

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73	gca	gat	gct	ggc	gac	cta	tcc	aga	atg	atc	aag	cat	ttt	aag	aag	caa	683
74	Ala	Asp	Ala	Gly	Asp	Leu	Ser	Arg	Met	Ile	Lys	His	Phe	Lys	Lys	Gln	
75	115					120				125							
77	aag	agg	cta	att	cct	gaa	aga	act	gtt	tgg	aag	tat	ttt	gtt	cag	ctt	731
78	Lys	Arg	Leu	Ile	Pro	Glu	Arg	Thr	Val	Trp	Lys	Tyr	Phe	Val	Gln	Leu	
79	130					135				140			145				
81	tgc	agt	gca	ttg	gaa	cac	atg	cat	tct	cga	aga	gtc	atg	cat	aga	gat	779
82	Cys	Ser	Ala	Leu	Glu	His	Met	His	Ser	Arg	Arg	Val	Met	His	Arg	Asp	
83						150				155			160				
85	ata	aaa	cca	gct	aat	gtg	ttc	att	aca	gcc	act	ggg	gtg	gta	aaa	ctt	827
86	Ile	Lys	Pro	Ala	Asn	Val	Phe	Ile	Thr	Ala	Thr	Gly	Val	Val	Lys	Leu	
87						165			170			175					
89	gga	gat	ctt	ggg	ctt	ggc	cgg	ttt	ttc	agc	tca	aaa	acc	aca	gct	gca	875
90	Gly	Asp	Leu	Gly	Leu	Gly	Arg	Phe	Phe	Ser	Ser	Lys	Thr	Thr	Ala	Ala	
91						180			185			190					
93	cat	tct	tta	gtt	ggt	acg	cct	tat	tac	atg	tct	cca	gag	aga	ata	cat	923
94	His	Ser	Leu	Val	Gly	Thr	Pro	Tyr	Tyr	Met	Ser	Pro	Glu	Arg	Ile	His	
95						195			200			205					
97	gaa	aat	gga	tac	aac	ttc	aaa	tct	gac	atc	tgg	tct	ctt	ggc	tgt	cta	971
98	Glu	Asn	Gly	Tyr	Asn	Phe	Lys	Ser	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Leu	
99	210					215			220			225					
101	cta	tat	gag	atg	gct	gca	tta	caa	agt	cct	ttc	tat	ggt	gac	aaa	atg	1019
102	Leu	Tyr	Glu	Met	Ala	Ala	Leu	Gln	Ser	Pro	Phe	Tyr	Gly	Asp	Lys	Met	
103						230			235			240					
105	aat	tta	tac	tca	ctg	tgt	aag	aag	ata	gaa	cag	tgt	gac	tac	cca	cct	1067
106	Asn	Leu	Tyr	Ser	Leu	Cys	Lys	Ile	Glu	Gln	Cys	Asp	Tyr	Pro	Pro		
107						245			250			255					
109	ctt	cct	tca	gat	cac	tat	tca	gaa	gaa	ctc	cga	cag	tta	gtt	aat	atg	1115
110	Leu	Pro	Ser	Asp	His	Tyr	Ser	Glu	Glu	Leu	Arg	Gln	Leu	Val	Asn	Met	
111						260			265			270					
113	tgc	atc	aac	cca	gat	cca	gag	aag	cga	cca	gac	gtc	acc	tat	gtt	tat	1163
114	Cys	Ile	Asn	Pro	Asp	Pro	Glu	Lys	Arg	Pro	Asp	Val	Thr	Tyr	Val	Tyr	
115						275			280			285					
117	gac	gta	gca	aag	agg	atg	cat	gca	tgc	act	gca	agc	agc	taaacatgca		1212	
118	Asp	Val	Ala	Lys	Arg	Met	His	Ala	Cys	Thr	Ala	Ser	Ser				
119						290			295			300					
121	agatcatgaa	gagtgttaacc	aaagtaattg	aaagtatttt	gtg	caaagtc	gtac	ctsc	ccc							1272	
123	atttatgtct	gggtgttaag	attaatattt	cagagctagt	gtg	ctctgaa	tc	ctta	acca							1332	
125	gttttcatat	aagcttcatt	tttgtaccgt	cacctaaatc	ac	tc	tc	tt	gc	aac	cccc	aaaa				1392	
127	tgactttgga	ataactgaat	tgc	atgttag	gag	aaaaat	gaa	acat	gt	ttttt	gaa	ttt	ttt	ttt	ttt	1452	
129	ggctaaaggt	ttatagaatt	tcttacagtt	ttctgctgtat	aa	att	gt	ttt	gtt	tag	at	at	at	at	at	1512	
131	gtc	agt	gcca	aat	att	gaag	gt	gc	ag	cc	at	tc	ac	ct	tg	aga	1572
133	aaa	agt	atct	ga	ac	at	gt	tg	ttt	ctt	ttt	ttt	ttt	ttt	ttt	ttt	1632
135	aca	att	gt	ga	act	ttt	ttt	t	ttt	aa	ac	ttt	ttt	ttt	ttt	ttt	1692
137	ttagc	ag	ttt	caaa	tat	gat	t	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1752
139	aac	at	ttt	ta	g	at	ct	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1812
141	gaca	aaa	at	gt	gt	g	at	gt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1872
143	tcttgcatt	gaa	at	gg	tat	aa	at	g	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1932
145	tgg	tgt	gata	ta	at	ttt	ta	a	gtt	gc	aca	ttt	ttt	ttt	ttt	ttt	1992

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147 tttttttttt acattttaaaa aatattcttt gaataacccctt gcagttactat atttcaagrt 2052  
 149 ttctttataa atttaagtgc attttaactc ataattgtac actataatat aagcctaagt 2112  
 151 ttttattcat aagttttattt gaagttctga tcggccccct tcagaaattt ttttatatta 2172  
 153 ttcttcaagt tactttctta tttatattgt atgtgcattt tatccattaa tgtttcatac 2232  
 155 tttctgagag tataataccc tttaaaaga tatttggat accaatactt ttcctggatt 2292  
 157 gaaaactttt tttaaacttt ttaaaatttgg gccactctg tatgcataatg tttggcttg 2352  
 159 tttaaaggagga agaaaggatg tgttttatac tgtacctgtg aatgttgcata cagttacaat 2412  
 161 ttatggaca aggttgcata tctagaatat gcttaataaa atgaaaactg gccatgacta 2472  
 163 cagccagaac ttttatgaga ttaacatttc tattgagaag cttttggat aagtactgt 2532  
 165 ttgttcatg aagatgactg agatggtaac acttcgtgt gcttaaggaa atgggcagaa 2592  
 167 ttctgtttttt gctgttgc agatgtgtt tccctgaatg ctttgcattt agtggcgacc 2652  
 169 agtttctcac agaattgtga agcctgaagg ccaagaggaa gtcactgtt aaggactctg 2712  
 171 tgccatctta caaccttggta tgaattatcc tgccaacgtg aaaacctcat gttcaaagaa 2772  
 173 cacttccctt tagccatgt aactgcttgt tttgttttc atatgtgtt ttcttacact 2832  
 W--> 175 catttgaatg ctttcaagca tttgtaaact taaaaaaaaan wawaaaggc aaaaagtctg 2892  
 177 aacccttgc ttctgaaatc taatcagtttta tgtatggttt ctgaaggta attttatattt 2952  
 179 ggaataggta aagcgaaacc tttttgtcw ttttttctt gagggttaga tgcattttt 3012  
 181 ttctcacact cttaatgact tttaacattt atactgagca tccatagata tattcctaga 3072  
 183 agtatgagaa gaattattct tattgaccat taatgtcatg ttcattttaa tgtaatataa 3132  
 185 ttgagatgaa atgttctctg gttggAACAG atactctttt tttttttttt gcaatctta 3192  
 187 agaatacata gatctaaaat tcattagctt gaccctcaa agtaactttt aagtaaagat 3252  
 189 taaagctttt cttctcagtg aatatatctg ctggaaatggaa atagctgggaa agaatttaat 3312  
 191 gatcagggaa attcattttt tctatatgtg gaaactttt gcttcgaata ttgtatctt 3372  
 193 ttaaatctaa atgttcatat tttcctgaa gaaaccactg tgtaaaaaatc aaatttaat 3432  
 195 ttgtatggaa ataatttcaa agaactatga agatgattt aagctctaattt ttatatagtc 3492  
 197 acctataaaaaa tttttttt atgtgttcat aagtaaattt tatattgatt aagttaaaact 3552  
 W--> 199 ttgtatggaa tttgaggagc agtaaaaatga aagctatatc tattnctaaa ccytatttag 3612  
 201 acattggkac cagttaccca ggtgaaaata kggagtaact ttgttttgc ttgtatgggtt 3672  
 W--> 203 taggaatggc ggatgaaggg tatctctata taaataaaatg gctcaacaat gtcaatgt 3732  
 205 tgtaaatttta gtaagatattt acagccattt catgaatgtt ttaccattca acatagtatc 3792  
 207 tattacaaaa cacctttctt gtatccatattt acttcagggtt ttgctgtttaa catttactat 3852  
 209 gatattttt ttaacccaaaaa tgctactcac attaaatgtt tattctttaa aatgaatgt 3912  
 211 ttatgtttttt aacccacaaaaa tgctacttta ccctgtgcct catattcaaa tagtactgt 3972  
 213 atatggacat ctttgcgtt aatcttttattttt tttgttatgc tttaaatata cataaaaaaa 4032  
 215 gatttctgtt attagcttttggaa aaaattgtat aatatcctaa tataacaaaaa atataaaaaat 4092  
 217 aaaaatgaat acagttaaaaa aaaaaaaaaaaaaa aaaaaaaaaaaaaa aaagg 4137  
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 222 <212> TYPE: PRT  
 223 <213> ORGANISM: Homo sapiens  
 225 <400> SEQUENCE: 2  
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 227 1 5 10 15  
 229 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala  
 230 20 25 30  
 232 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val  
 233 35 40 45  
 235 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys  
 236 50 55 60

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Input Set : N:\Crf3\RULE60\09757982.txt  
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238 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile  
 239 65 70 75 80  
 241 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys  
 242 85 90 95  
 244 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu  
 245 100 105 110  
 247 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys  
 248 115 120 125  
 250 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln  
 251 130 135 140  
 253 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg  
 254 145 150 155 160  
 256 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys  
 257 165 170 175  
 259 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala  
 260 180 185 190  
 262 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile  
 263 195 200 205  
 265 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys  
 266 210 215 220  
 268 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys  
 269 225 230 235 240  
 271 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro  
 272 245 250 255  
 274 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn  
 275 260 265 270  
 277 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val  
 278 275 280 285  
 280 Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser  
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 286 <212> TYPE: DNA  
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 290 <221> NAME/KEY: CDS  
 291 <222> LOCATION: (1)..(906)  
 293 <400> SEQUENCE: 3  
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 295 Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe  
 296 1 5 10 15  
 298 caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc 96  
 299 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala  
 300 20 25 30  
 302 aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt 144  
 303 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val  
 304 35 40 45  
 306 tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa 192  
 307 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys

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308	50	55	60	
310	gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc			240
311	Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile			
312	65	70	75	80
314	aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa			288
315	Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys			
316	85	90	95	
318	tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa			336
319	Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu			
320	100	105	110	
322	cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag			384
323	Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys			
324	115	120	125	
326	caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag			432
327	Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln			
328	130	135	140	
330	ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga			480
331	Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg			
332	145	150	155	160
334	gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa			528
335	Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys			
336	165	170	175	
338	ctt gga gat ctt ggg ctt ggc cggtttttc agc tca aaa acc aca gct			576
339	Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala			
340	180	185	190	
342	gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata			624
343	Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile			
344	195	200	205	
346	cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt			672
347	His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys			
348	210	215	220	
350	cta cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa			720
351	Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys			
352	225	230	235	240
354	atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca			768
355	Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro			
356	245	250	255	
358	cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat			816
359	Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn			
360	260	265	270	
362	atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt			864
363	Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val			
364	275	280	285	
366	tat gac gta gca aag agg atg cat gca tgc act gca agc agc			
367	Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser			
368	290	295	300	
371	<210> SEQ ID NO: 4			
372	<211> LENGTH: 2120			
373	<212> TYPE: DNA			

**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\09757982.txt  
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L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1